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Q7 61 PAVAVATGTHLIVAVKSRVYMDIDRSLRERLEATLQAVTLHAWWTHGADRALIL 120
DB 61 PAVAVATGTHLIVAVKSRVYMDIDRSLRERLEATLQAVTLHAWWTHGADRALIL 120
Q7 121 DQVTRVYHRSVYALRKHGVSQVWNLGHSQVGAISLQVYIALHSEKVKNIATVWTPVDFQ 180
DB 121 DQVTRVYHRSVYALRKHGVSQVWNLGHSQVGAISLQVYIALHSEKVKNIATVWTPVDFQ 180
Q7 121 DQVTRVYHRSVYALRKHGVSQVWNLGHSQVGAISLQVYIALHSEKVKNIATVWTPVDFQ 180
DB 121 DQVTRVYHRSVYALRKHGVSQVWNLGHSQVGAISLQVYIALHSEKVKNIATVWTPVDFQ 180
Q7 181 TQNLISAWVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 240
DB 181 TQNLISAWVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAV 240
Q7 241 PHTLHAWWTHGADRALIL 120 PHTLHAWWTHGADRALIL 120 PHTLHAWWTHGADRALIL 120 400
DB 241 PHTLHAWWTHGADRALIL 120 PHTLHAWWTHGADRALIL 120 PHTLHAWWTHGADRALIL 120 400
Q7 301 MOHUVHPDASKALALHLSSTSDYTELAPGGHGGIYVSKAQGVVDAFGHWNERG 357
DB 301 MOHUVHPDASKALALHLSSTSDYTELAPGGHGGIYVSKAQGVVDAFGHWNERG 357
RESULT 2
US-09-756-417-4
Sequence 4, Application US/08756317
Patent No. 5849894
GENERAL INFORMATION:
APPLICANT: Clemente, Thomas E.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Miskay, Timothy A.
APPLICANT: Stark, David M.
TITLE OF INVENTION: Improved Rhodospirillum rubrum
TITLE OF INVENTION: Poly-D-hydroxyalkanoate Synthesis
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Barker
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/756-417
FILING DATE: 25 NOV-1996
CLASSIFICATION: C12
PRIORITY INFORMATION:
APPLICATION NUMBER: US 60/007,694
FILING DATE: 29 NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/BOOK NUMBER: 16461008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1440
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 674 amino acids
TYPE: amino acid
STANDARD: 1
TOPLOGY: linear
US-09-756-417-4

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Query Match 15.4% Score 297.5; DB 2; Length 574;
Pair Local Similarity 25.9%; Pct. Ident. 22;
Matches 97; Mismatches 51; Gaps 16;

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Q7 311 PHTLHAWWTHGADRALIL 120 PHTLHAWWTHGADRALIL 120 PHTLHAWWTHGADRALIL 120 45
DB 181 LQAVTLHAWWTHGADRALIL 120 LQAVTLHAWWTHGADRALIL 120 LQAVTLHAWWTHGADRALIL 120 45
Q7 66 LQAVTLHAWWTHGADRALIL 120 LQAVTLHAWWTHGADRALIL 120 LQAVTLHAWWTHGADRALIL 120 125
DB 66 LQAVTLHAWWTHGADRALIL 120 LQAVTLHAWWTHGADRALIL 120 LQAVTLHAWWTHGADRALIL 120 125
Q7 226 VHERLLAVVETWAKYITGLPERKGLKRVHVDQGVAVVQWNVFAGLAEETHEELIS 285
DB 226 VHERLLAVVETWAKYITGLPERKGLKRVHVDQGVAVVQWNVFAGLAEETHEELIS 285
Q7 126 QVDEGVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 181
DB 126 QVDEGVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 181
Q7 286 QGPLAAVMETDQRAVLGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVV 345
DB 286 QGPLAAVMETDQRAVLGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVV 345
Q7 182 PGNILSARVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 248
DB 182 PGNILSARVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 248
Q7 346 PGL LQAVTLHAWWTHGADRALIL 120 PGL LQAVTLHAWWTHGADRALIL 120 PGL LQAVTLHAWWTHGADRALIL 120 400
DB 346 PGL LQAVTLHAWWTHGADRALIL 120 PGL LQAVTLHAWWTHGADRALIL 120 PGL LQAVTLHAWWTHGADRALIL 120 400
Q7 230 VVWNT PHTLHAWWTHGADRALIL 120 VVWNT PHTLHAWWTHGADRALIL 120 VVWNT PHTLHAWWTHGADRALIL 120 297
DB 230 VVWNT PHTLHAWWTHGADRALIL 120 VVWNT PHTLHAWWTHGADRALIL 120 VVWNT PHTLHAWWTHGADRALIL 120 297
Q7 401 KIPAAFTLLYWNHGTETMEFAAMQVYVTEFMVQENKLVQVQKLTWIAHLLERTRIVAVL 460
DB 401 KIPAAFTLLYWNHGTETMEFAAMQVYVTEFMVQENKLVQVQKLTWIAHLLERTRIVAVL 460
Q7 298 VVWNT PHTLHAWWTHGADRALIL 120 VVWNT PHTLHAWWTHGADRALIL 120 VVWNT PHTLHAWWTHGADRALIL 120 342
DB 298 VVWNT PHTLHAWWTHGADRALIL 120 VVWNT PHTLHAWWTHGADRALIL 120 VVWNT PHTLHAWWTHGADRALIL 120 342
Q7 461 USABHGHAWWTHGADRALIL 120 USABHGHAWWTHGADRALIL 120 USABHGHAWWTHGADRALIL 120 519
DB 461 USABHGHAWWTHGADRALIL 120 USABHGHAWWTHGADRALIL 120 USABHGHAWWTHGADRALIL 120 519
Q7 443 PHTLHAWWTHGADRALIL 120 PHTLHAWWTHGADRALIL 120 PHTLHAWWTHGADRALIL 120 45
DB 443 PHTLHAWWTHGADRALIL 120 PHTLHAWWTHGADRALIL 120 PHTLHAWWTHGADRALIL 120 45
Q7 528 KAWLISATPHLAKSW 533
DB 528 KAWLISATPHLAKSW 533
RESULT 3
US-09-756-417-3
Sequence 3, Application US/08756317
Patent No. 5849894
GENERAL INFORMATION:
APPLICANT: Clemente, Thomas E.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Miskay, Timothy A.
APPLICANT: Stark, David M.
TITLE OF INVENTION: Improved Rhodospirillum rubrum
TITLE OF INVENTION: Poly-D-hydroxyalkanoate Synthesis
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Barker
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/756-417
FILING DATE: 25 NOV-1996
CLASSIFICATION: C12
PRIORITY INFORMATION:
APPLICATION NUMBER: US 60/007,694
FILING DATE: 29 NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/BOOK NUMBER: 16461008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1440
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 600 amino acids
TYPE: amino acid
STANDARD: 1
TOPLOGY: linear
US-09-756-417-3

```


Patent No. 5,210,004
GENERAL INFORMATION:
APPLICANT: Clemente, Thomas E.
APPLICANT: Kishore, Ganesh M.
ATTORNEY: Marky, Timothy A.
APPLICANT: Stark, David M.
TITLE OF INVENTION: Improved Method of Detecting
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Burke
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/007,756, 417
FILING DATE: 25-Nov-1996
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
PRIORITY NUMBER: 03/407,053
FILING DATE: 29-Nov-1995
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, McIndoo L.
REGISTRATION NUMBER: 13,062
REFERENCE/DOCKET NUMBER: M 1008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NOs 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: Linear
ORF 756, 117-5

Query Match 14.06; Score 24.45; 18.4; Length 589
Best Local Similarity 26.06; Field No. 4.24; 2.3
Matches 97; Conservative 98; Mismatches 157; Gaps 14

QY 24 TGGGNNLL...KADG...-...TGVTHVVRVVRKIVIVHYRPAALVAIUF 68
DB 179 LRAGVNMHRLKGLSGLISAEIVIRVAVTEAAVVEHYVETLQYKPLIKVHA 207
QY 65 TELLVAAVNRPMTHLDRSTTKHIAIDQWYTHWYTHGADRAITLDTINYYI 128
DB 239 KLLLVVPTINKYVLLQLHESLVSRNHWVQTHVTVVAKRRIQAAMAGSTWGTTHAA 297
QY 129 DRVVTPLRTHWQVNIQLHGLVSSAF SIVYTAHSEKVENIATVVPVIDIQTION 184
DB 296 LRATVARGDSQKINVLGTVGGTIVSTALAVAAAGLHAASVITLTLGLAHTG 406
QY 186 ELASVQVNVIVAVVIMKNTIT...ELAVPLKPKETETLKVVRVRLID 200
DB 357 TLAVFVLEAVVQPEALHGGVAVAPALVGLLALANLSETEKNCIVWRIV 407
QY 256 DELRVNTER-----MEKRIEUSEAVDTEFQFANLQEPNINQAVLIDLEV 200
DB 408 -VIVLTKENTIVTTLTETNRKATNLTPTWYVWYVETLNEKVKETLWVWIV 463
QY 287 DLKRTTGLVAGGGLHAGGVAAGSSNAAVAGSSNAAVAGSSNAAVAGSSNAAV 546
DB 464 DLASTIVPTIVYSREHIVPWIAAYASALLAN...KSLIVIGASTHIVAVINPAK 100
QY 447 PATGRVINE 155

14.44; Score 24.45; 18.4; Length 589
26.06; Field No. 4.24; 2.3
Matches 97; Conservative 98; Mismatches 157; Gaps 14
QY 24 TGGGNNLL...KADG...-...TGVTHVVRVVRKIVIVHYRPAALVAIUF 68
DB 179 LRAGVNMHRLKGLSGLISAEIVIRVAVTEAAVVEHYVETLQYKPLIKVHA 207
QY 65 TELLVAAVNRPMTHLDRSTTKHIAIDQWYTHWYTHGADRAITLDTINYYI 128
DB 239 KLLLVVPTINKYVLLQLHESLVSRNHWVQTHVTVVAKRRIQAAMAGSTWGTTHAA 297
QY 129 DRVVTPLRTHWQVNIQLHGLVSSAF SIVYTAHSEKVENIATVVPVIDIQTION 184
DB 296 LRATVARGDSQKINVLGTVGGTIVSTALAVAAAGLHAASVITLTLGLAHTG 406
QY 186 ELASVQVNVIVAVVIMKNTIT...ELAVPLKPKETETLKVVRVRLID 200
DB 357 TLAVFVLEAVVQPEALHGGVAVAPALVGLLALANLSETEKNCIVWRIV 407
QY 256 DELRVNTER-----MEKRIEUSEAVDTEFQFANLQEPNINQAVLIDLEV 200
DB 408 -VIVLTKENTIVTTLTETNRKATNLTPTWYVWYVETLNEKVKETLWVWIV 463
QY 287 DLKRTTGLVAGGGLHAGGVAAGSSNAAVAGSSNAAVAGSSNAAVAGSSNAAV 546
DB 464 DLASTIVPTIVYSREHIVPWIAAYASALLAN...KSLIVIGASTHIVAVINPAK 100
QY 447 PATGRVINE 155

14.44; Score 24.45; 18.4; Length 589
26.06; Field No. 4.24; 2.3
Matches 97; Conservative 98; Mismatches 157; Gaps 14
QY 24 TGGGNNLL...KADG...-...TGVTHVVRVVRKIVIVHYRPAALVAIUF 68
DB 179 LRAGVNMHRLKGLSGLISAEIVIRVAVTEAAVVEHYVETLQYKPLIKVHA 207
QY 65 TELLVAAVNRPMTHLDRSTTKHIAIDQWYTHWYTHGADRAITLDTINYYI 128
DB 239 KLLLVVPTINKYVLLQLHESLVSRNHWVQTHVTVVAKRRIQAAMAGSTWGTTHAA 297
QY 129 DRVVTPLRTHWQVNIQLHGLVSSAF SIVYTAHSEKVENIATVVPVIDIQTION 184
DB 296 LRATVARGDSQKINVLGTVGGTIVSTALAVAAAGLHAASVITLTLGLAHTG 406
QY 186 ELASVQVNVIVAVVIMKNTIT...ELAVPLKPKETETLKVVRVRLID 200
DB 357 TLAVFVLEAVVQPEALHGGVAVAPALVGLLALANLSETEKNCIVWRIV 407
QY 256 DELRVNTER-----MEKRIEUSEAVDTEFQFANLQEPNINQAVLIDLEV 200
DB 408 -VIVLTKENTIVTTLTETNRKATNLTPTWYVWYVETLNEKVKETLWVWIV 463
QY 287 DLKRTTGLVAGGGLHAGGVAAGSSNAAVAGSSNAAVAGSSNAAVAGSSNAAV 546
DB 464 DLASTIVPTIVYSREHIVPWIAAYASALLAN...KSLIVIGASTHIVAVINPAK 100
QY 447 PATGRVINE 155

QY 447 PATGRVINE 155

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10 2 EPIIDHRELLI...
 11 63 QVATOTPHLLI...
 12 62 ACP...
 13 61 Y...
 14 60 Y...
 15 59 Y...
 16 58 Y...
 17 57 Y...
 18 56 Y...
 19 55 Y...
 20 54 Y...
 21 53 Y...
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 24 50 Y...
 25 49 Y...
 26 48 Y...
 27 47 Y...
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 91 0 Y...
 92 0 Y...
 93 0 Y...
 94 0 Y...
 95 0 Y...
 96 0 Y...
 97 0 Y...
 98 0 Y...
 99 0 Y...
 100 0 Y...

10 2 EPIIDHRELLI...
 11 63 QVATOTPHLLI...
 12 62 ACP...
 13 61 Y...
 14 60 Y...
 15 59 Y...
 16 58 Y...
 17 57 Y...
 18 56 Y...
 19 55 Y...
 20 54 Y...
 21 53 Y...
 22 52 Y...
 23 51 Y...
 24 50 Y...
 25 49 Y...
 26 48 Y...
 27 47 Y...
 28 46 Y...
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 46 28 Y...
 47 27 Y...
 48 26 Y...
 49 25 Y...
 50 24 Y...
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 67 7 Y...
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 70 4 Y...
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 72 2 Y...
 73 1 Y...
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 93 0 Y...
 94 0 Y...
 95 0 Y...
 96 0 Y...
 97 0 Y...
 98 0 Y...
 99 0 Y...
 100 0 Y...

Cell Motil. Cytoskeleton 32:24-46(1995).

1-1 FUNCTIONAL LENGTH HAS ACTIVE ACTIVITY, REPLACING LENGTH AS A MEASURE FOR THE INTERMEDIATE DIFFUSION MOBILITY OF VESICLES AND ORGANELLES ALONG MICROTUBULES

1 SUBUNIT COMPOSED OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF INTERMEDIATE AND LIGHT CHAINS.

1-1 SUBCELLULAR LOCATION: Cytoplasmic.

1 SIMILARITY, BELONGS TO THE DYNER HEAVY CHAIN FAMILY.

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[1]
CCCCC CCCC FROM N.A.
CCCCC KEG
CCCCC EICMAN 6018 9789; TRANSPOSER TMS52;
CCCCC MPN1MP-61014696; Patent 2170815;
CCCCC Biological Science, G.H.;
CCCCC "TMS52; a novel transposable element from Staphylococcus aureus";
CCCCC Engl. Microbiol. 4:961-975(1990).
CCCCC -----
CCCCC This SWISS-Pat entry is copyright. It is produced through a collaboration
CCCCC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CCCCC modified and this statement is not removed, changed by and/or commercial
CCCCC entities requiring a license agreement. The following shall have no effect
CCCCC or secondarily affect the use of said entry.
CCCCC -----
CCCCC EMBL: X52734; GNA36949.1; .
CCCCC DR
CCCCC PIR: S11780;
CCCCC DR
CCCCC InterPro: IPR001584; Rve.
CCCCC DR
CCCCC Pfam: PF00665; rve; 1.
CCCCC DR
CCCCC Transposable element, Transposon; DNA binding, DNA recombination.
CCCCC DR
CCCCC DNA_BIND 36 45 H-T H motif (POTENTIAL);
CCCCC FT
CCCCC SEQUENCE 480 AA; 5631 MW; DFC0835CA7B8C4BB CRC64;

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[illegible][illegible]

RESULT	14				
LIP_PSEGL					
LIP	15	LIP_PSEGL	STANDARD;	PRT;	458 AA.
AC	005489;				
DET	01-0576-1994	(01. 30, Created)			
DT	01-OCT-1994	(01. 30, Last sequence update)			
DE	15-MI-1999	(01. 38, Last annotation update)			
EN	Lipase precursor	(EC 3.1.1.3) (Triacylglycerol lipase).			
LN	LIP				

Chromobacterium viscosum.
Bacteria: Proteobacteria: beta subdivision: Burkholderia group:
Burkholderia.
BFL-3231, 1279;
[1]
SOURCE FROM N.A., SPECIES OF 4.6, AND MUTAGENESIS.
SPECIES-P. glumae; STRAIN-PGL / CBS 322.89;
BFLINE 9319193, PABED 1476423;
FROEDER, D.C., LEMOND, H.E., BATEMAN, A.M., BOE, J.W., VISSER, C.,
VERRIPS, C.T.;
"Cloning of the Pseudomonas glumae lipase gene and determination of
the catalytic site residues";
APPL. ENVIRON. MICROBIOL. 59, 3757-3763 (1993).

Cell Motil. Cytoskeleton 32:24-46(1995).

-1- FUNCTION: LEMN1 HAS ACTIN ACTIVITY, AND PLAYS A KEY ROLE IN THE INTRACELLULAR MOTILITY OF VESICLES AND ORGANELLES ALONG MICROTUBULES

-1 SUBUNIT COMPOSED OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF INTERMEDIATE AND LIGHT CHAINS.

-1 SUBCELLULAR LOCATION: Cytoplasmic.

-1 SIMILARITY: BELONGS TO THE DYERIN HEAVY CHAIN FAMILY.

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[1]
CCCCC CCCC FROM N.A.
CCCCC KEG
CCCCC EICMAN 6018 9789; TRANSPOSER T8552;
CCCCC MPB11NP-6101466; Patent 2170815;
CCCCC Biological Science & Tech.;
CCCCC "T8552; a novel transposable element from Staphylococcus aureus.";
CCCCC Engl. Microbiol. 4:961-975(1990).
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CCCCC EMBL: X52734; GNA36949.1; .
CCCCC DR
CCCCC PIR: S11780;
CCCCC DR
CCCCC InterPro: IPR001584; Rve.
CCCCC DR
CCCCC Pfam: PF00665; rve; 1.
CCCCC DR
CCCCC Transposable element, Transposon; DNA binding, DNA recombination.
CCCCC DR
CCCCC DNA_BIND 36 45 H-T H motif (POTENTIAL);
CCCCC FT
CCCCC SEQUENCE 480 AA; 5631 MW; DFC0835CA7B8C4BB CRC64;

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Query Match	5.4%	Score 101	DB 1	Length 480								
Best local similarity	21.7%	Fred. No. 1.4										
Matches 53	Conservative 32	Mismatches 61	Indels 98	Gaps 11								
59	1	TRDAV	HAERLVLRV	...	SGGAAVATCTTLLIVAG	VRLVMTDI	86					
61	3	TRAVT	TEHREHQA	REVLTL	TEHSEHSE	QWALHLLV	YVGG	QTHRPQMTLL	189			
62	27	LEELA	TEELALIVL	LVWYPT	QAEALTEFL	...	RAYL	DEQVY	LEH	179		
63	130	MEGSKAFAG	...	YVSTLAF	RAAG	NTLHQA	WURRT	TRMVA	YGLT	KEPVIDH	241	
64	135	AVQAN	LVTL	GLAET	LVTL	ESLQVGR	QWHTV	TV	STNHL	LSAAG	KVQV	189

[illegible]

RESULT	14				
LIP_PSEGL					
LIP	15	LIP_PSEGL	STANDARD	PRT	458 AA.
AC	005489				
DET	01-0276-1994	(01.30, Created)			
DT	01-OCT-1994	(01.30, Last sequence update)			
DE	15-MAR-1999	(01.38, Last annotation update)			
DE		Lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).			
DN					
LIP					

Chromobacterium viscosum.
Bacteria: Proteobacteria: beta subdivision: Burkholderia group:
Burkholderia.
BFL-3237, 1279;
[1]
SOURCE FROM N.A., SPECIES OF 4.0, AND MUTAGENESIS.
SPECIES-P. glumae; STRAIN-PGL / CBS 322.89;
BFLINE 9319193, PABED 1476423;
TRENKLE H.C., LEMOND H.E., BATEMAN A.M., BOE J.W., VISSER C.J.,
VERRIPS C.T.;
"Cloning of the Pseudomonas glumae lipase gene and determination of
the catalytic site residues";
APPL. ENVIRON. MICROBIOL. 59, 3757-3763 (1993).

RC STRAIN DSM1124 (ALC 29714)
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 RI 96 Local Similarity 24.98; Pred. No. 2,26-15;
 P2 100 Matches 96; Conservation 60; Mismatches 174; Gaps 0;
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Query Match
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 Matches 96; Conservation 60; Mismatches 174; Gaps 0;
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 P100 100 Gaps 0;


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DR InterPro: IPR000873; AMP bind.
DR InterPro: IPR000879; Est_Hlp_diest_act site.
DR InterPro: IPR00734; Lipase.
DR Pfam: PF00601; AMP binding 3.
DR PROSITE: PROSITE: LIPASE_SIB; BKNAN_L.
KW Hypothetical protein.
SQ SEQUENCE 1016 AA; 109182 MW; 010720519678300 CR664;

Query Match 14.2% Score 267; DC 2; Length 1016;
best local similarity 27.2%; Pred. No. 2,24-13;
Matches 101; Conservation 60; Mismatches 171; Indels 40; Gaps 16;

29 4 EDDIDRPPKLLHMDLLEKELRRLKELKSLV VTEHAYVELLKLATGTRRP 61
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46 19 ESTVTP---VERVATAQ--RHETVREGGHEETETTSNSQIVGVVYKLRKPTP 71
   | | | | | | | | | | | | | | | | | | | | | | | | | |
59 62 AAVATQVLL PELVATALVRIINTEIQERKATKRLATGGAVLLHWYTFQALRAL 118
   | | | | | | | | | | | | | | | | | | | | | | | | | |
66 72 GRRFEPFLDAIVLVHPPMRGAPKQVTHHNAVHLENTROLVWVHDSPTKVTDM 141
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79 119 -LLLDQINSHYLRKVDLRLHVLQVNLDSVQDAFSQNTAL RLKRNELVIM 173
   | | | | | | | | | | | | | | | | | | | | | | | | | |
86 132 LRLALHVA LELAVTVELVINE VHVTVVYGRF CYQAAZYHETRIASIVAF 187
   | | | | | | | | | | | | | | | | | | | | | | | | | |
93 174 VLPVDFDPLDGLSAWV-KVAVLA VQDGR LLRLSRHSKQFLDQKY 227
   | | | | | | | | | | | | | | | | | | | | | | | | | |
100 189 -GVV- LLAATPMELTRF NVLAREMGRDRLHLLVLAASLDELLE LFAR 244
   | | | | | | | | | | | | | | | | | | | | | | | | | |
107 229 VRNV LLLETRVVERDMEERLLELQALTEESLSTEDENNTNVALI 281
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114 245 VQVPLQHNKREALGRDQLERHLESLAWG--GLATSELLESLAHSRSMLEAV 300
   | | | | | | | | | | | | | | | | | | | | | | | | | |
121 282 GQGVVGRRLFTVRLHPLHLVLLALALA-LTGLHLYTTRDITGRLGNTVQSEA 341
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128 301 KEMVTLGLLGLTFLAVHAYVGLQGLAVSTGLGAAINAEVTEELTKTRHFLAVSRA 360
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135 322 GGVTHFALGRWL 353
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142 361 AGSWPLVAVNV 372

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Search completed: July 20, 2002, 05:01:15
 Job time: 824 sec

PR		US 6,001,879 A1
XX		
XX		
XX	26 JUL 2001	
XX		
XX	26 DEC 2000; 2000WO US 4426 X.	
XX		
XX	21 JAN 2000; 2000RS 0149725,	
XX	25 APR 2000; 2000RS 0552117,	
PR	09 JUN 2000; 2000RS 0596042,	
PR	19 JUL 2000; 2000RS 0620312,	
PR	03 AUG 2000; 2000RS 0654450,	
PR	14 SEP 2000; 2000RS 0662191,	
PR	19 OCT 2000; 2000RS 0694036,	
PR	29 NOV 2000; 2000RS 0727444,	
XX	(BYSEQ) HYSEQ INP.	
XX		
XX	Liu Q Y., Chen J., Li C F., Wu Y., Fan M., Guo L, Wang D,	
P1	Wang J., Wang Z., Weidong T., Xu C G., Yao A L., Yang Y., Zhang J;	
P1	Zhao Q A., Zhou P., Goodrich K., Brannan RT;	
XX		
XX	WP1 : 2001 442254/47.	
XX	N FSDb: AA156407.	
XX		
P1	Neuro nucleic acids and polypeptides, useful for treating disorders	
P1	such as central nervous system injury.	
XX		
XX	Paraq v 4.0 by H. R. 2006, 1997qf, Paraq Inc.	
XX		
XX	The invention relates to human nucleic acids (AA157796-AA161409) and	
CC	the encoded polypeptides (AA159612-AA162219) with localizing,	
CC	immunoprecipitant and cytoskeletal activity. The polypeptides are useful	
CC	in gene therapy. A composition containing a polypeptide or polynucleotide	
CC	of the invention may be used to treat diseases of the peripheral nervous	
CC	system, such as peripheral nervous injuries, peripheral neuropathy and	
CC	localized neuropathies and central nervous system diseases, such as	
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic	
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the	
CC	utilization of the invention in the treatment of nerve growth defects,	
CC	AIDS, HIV infection, bone marrow transplantation, stroke, trauma,	
CC	and thromboembolic activity, cancer diagnosis and therapy, drug screening,	
CC	CNS disorders,	
CC	assays for receptor activity, arthritis and inflammation, leukemias and	
CC	CNS disorders.	
CC	Note: The sequence data for this patent did not form part of the printed	
CC	Specification.	
XX		
XX	Sequence 439 AA.	
XX		

[illegible][illegible]



EA Martini B.N., Adairya A.G., Miska G.M., Fritwell T., Fitchell V.A.,
 F1 "The complete amino acid sequence of a biologically active
 F2 1-77 residue fragment of M protein isolated from type 5 group A
 F3 streptococcus".
 F4 J. Biol. Chem. 259:3666-3669(1984).
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